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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/804,615

DATE: 08/15/2001

TIME: 08:22:46

Input Set : A:\Bgn-111.app

Output Set: N:\CRF3\08132001\I804615.raw

ENT 0.000

3 <110> APPLICANT: Johansen, Teit E.  
 4       Wen-Yee Saw, Dinah  
 6 <120> TITLE OF INVENTION: Novel Neurotrophic Factors  
 8 <130> FILE REFERENCE: Novel Neurotrophic Factors  
 10 <140> **CURRENT APPLICATION NUMBER: US/09/804,615**  
 11 <141> CURRENT FILING DATE: 2001-03-12  
 12 <150> PRIOR APPLICATION NUMBER: DANISH 1998 00904  
 14 <151> PRIOR FILING DATE: 1998-07-06  
 16 <150> PRIOR APPLICATION NUMBER: USSN 60/092,229  
 17 <151> PRIOR FILING DATE: 1998-07-09  
 19 <150> PRIOR APPLICATION NUMBER: DANISH 1998 01048  
 20 <151> PRIOR FILING DATE: 1998-08-19  
 21 <150> PRIOR APPLICATION NUMBER: USSN 60/097,774  
 23 <151> PRIOR FILING DATE: 1998-08-25  
 25 <150> PRIOR APPLICATION NUMBER: USSN 60/103,908  
 26 <151> PRIOR FILING DATE: 1998-10-13  
 28 <150> PRIOR APPLICATION NUMBER: DANISH 1998 01265  
 29 <151> PRIOR FILING DATE: 1998-10-06  
 31 <150> PRIOR APPLICATION NUMBER: U.S.S.N 09/347,613  
 32 <151> PRIOR FILING DATE: 1999-07-02  
 34 <160> NUMBER OF SEQ ID NOS: 40  
 36 <170> SOFTWARE: PatentIn Ver. 2.1  
 38 <180> SEQ ID NO: 1  
 39 <110> LENGTH: 865  
 40 <210> TYPE: DNA  
 41 <213> ORGANISM: Homo sapiens  
 43 <216> FEATURE:  
 44 <211> NAME/KEY: CDS  
 45 <212> LOCATION: 120)..(719)  
 47 <216> FEATURE:  
 48 <211> NAME/KEY: 5'UTR  
 49 <212> LOCATION: 1)..(119)  
 51 <216> FEATURE:  
 52 <211> NAME/KEY: 3'UTR  
 53 <212> LOCATION: 121)..(865)  
 55 <216> FEATURE:  
 56 <211> NAME/KEY: six\_peptide  
 57 <212> LOCATION: 120)..(170)  
 59 <216> FEATURE:  
 60 <211> NAME/KEY: mat\_peptide  
 61 <212> LOCATION: 145)..(719)  
 63 <216> FEATURE:  
 64 <211> NAME/KEY: misc\_structure  
 65 <212> LOCATION: 601)..(660)  
 66 <223> OTHER INFORMATION: CARBOHYD: Glycylated Asparagine at Asn57  
 67 <223> FEATURE:  
 68 <221> NAME/KEY: misc\_structure

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/804,615

DATE: 08/15/2011

TIME: 16:22:46

Input Set : A:\Bgn-111.app

Output Set: N:\CRF3\08132001\I804615.raw

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70 <222> LOCATION: (420)..(423)
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75 <223> OTHER INFORMATION: DISULFID: Cys4-Cys101 disulfide bridge
76 <223> FEATURE:
77 <221> NAME/KEY: misc_structure
78 <222> LOCATION: (519)..(513)
79 <223> OTHER INFORMATION: DISULFID: Cys19-Cys103 disulfide bridge
80 <223> FEATURE:
81 <221> NAME/KEY: misc_structure
82 <222> LOCATION: (616)..(619)
83 <223> OTHER INFORMATION: DISULFID: Cys72-Cys72 interchain disulfide bridge
84 <400> SEQUENCE: 1
85 ctatggagccc atgcccggcc tgatctcagc ccgaggacag cccctcccttg aggtccctcc 60
86 tcccaagcc caccctgggtg cctctcttct ccttgaggtt ccaattgggtc tctccgggc 119
87 atg cct gcc ctg tgg ccc acc ctg gcc gct ctg gct ctg ctg agc agc 167
88 Met Pro Ala Leu Trp Pro Thr Leu Ala Ala Leu Ala Leu Ser Ser
89 -45 -90 -85 -80
90 gtc gcc gag gcc tcc ctg gcc tcc ggc ccc ccc agc cct gcc ccc ggc 215
91 Val Ala Glu Ala Ser Leu Gly Ser Ala Pro Arg Ser Pro Ala Pro Arg
92 -75 -1 -65
101 aca gcc ccc ccg cct gtc ctg ggc tcc acc gcc agc ccc ctg ccg ggc 263
102 Glu Gly Pro Pro Val Leu Ala Ser Pro Ala Gly His Leu Pro Gly
103 -60 -55 -50
105 gga cgc acg gcc cgc tgg tgc agt gga aga gcc cgg cgg ccg cgc cgc 311
106 Gly Arg Thr Ala Arg Trp Cys Ser Gly Arg Ala Arg Arg Pro Arg Arg
107 -45 -40 -35
109 aca ccc ttc tgc gcc cgc gcc ccc gcc gcc tgc acc ccc atc tgc tct 359
110 Arg His Phe Ser Ala Arg Ala Pro Ala Ala Cys Thr Pro Ile Cys Ser
111 -30 -25 -20
113 tcc ccg cgg gtc cgc gcc gcc cgg ctg ggg gcc cgg gcc gcc ggc ctg 407
114 Ser Pro Arg Val Arg Ala Ala Arg Leu Gly Gly Arg Ala Ala Arg Ser
115 -15 -10 -5 -1 1
117 ggc agc ggg ggc gcc gcc tcc cgc ctg gcc tgc gag ctg ctg ccg gtc 455
118 Gly Ser Gly Gly Ala Gly Cys Arg Leu Arg Ser Glu Leu Val Pro Val
119 5 10 15
121 ggc gcc ctg gcc ctg gcc gcc gcc tcc gcc gcc ctg ggc cct gtc gtc 503
122 Arg Ala Leu Gly Leu Gly His Arg Ser Asp Ala Leu Val Arg Phe Arg
123 20 25 30
125 ttc tgc acc gcc tcc tcc gcc gcc gcc gcc gcc gcc gcc gcc gcc gcc 551
126 Phe Cys Thr Gly Ser Cys Pro Arg Ala Arg Ser Ser His Asp Leu Ser
127 35 40 45
129 ctg gcc acc gca ctg gcc gcc gcc gcc gcc gcc gcc gcc gcc gcc gcc 600
130 Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser
131 50 55 60 65
133 ggc gcc gcc gcc gcc gcc gcc gcc gcc gcc gcc gcc gcc gcc gcc gcc 647
134 Arg Pro Val Ser His Pro Cys Cys Arg His Thr Arg Tyr His Ala Val

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/804,615

DATE: 04-10-2001

TIME: 10:10

Input File : A:\Bgn-111.app

Output File: N:\CRF3\08132001\I804615.raw

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135
137 tcc ttc atg gac gtc aac agc acc ttc att att gtc gac agc atc ttc 840
138 Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val Asp Arg Leu Ser
139 85 87 88
141 gac acc acc ttc ggc tgc ctg ggc gga ggc ttc ggc agc agc ttc 840
142 Ala Thr Ala Cys Gly Cys Leu Gly
143 100 105
144 gaccctacc gagggtctt cctgctggg ggc ggc ggc ggc ggc ggc ggc ggc 840
145 cctcagccag ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc 865
146 <210> SEQ ID NO: 2
147 <211> LENGTH: 200
148 <212> TYPE: PRT
149 <213> ORGANISM: Homo sapiens
150 <400> SEQUENCE: 2
151 Met Pro Ala Leu Trp Pro Thr Leu Ala Ala Leu Ala Leu Leu Ser Ser
152 -95 -90 -85 -80
153 Val Ala Glu Ala Ser Leu Gly Ser Ala Pro Arg Ser Pro Ala Pro Arg
154 -75 -70 -65
155 Glu Gly Pro Pro Pro Val Leu Ala Ser Pro Ala Gly His Leu Pro Gly
156 -60 -55 -50
157 Gly Arg Thr Ala Arg Trp Cys Ser Gly Arg Ala Arg Arg Pro Arg Arg
158 -45 -40 -35
159 Arg His Phe Ser Ala Arg Ala Pro Ala Ala Cys Thr Pro Ile Cys Ser
160 -30 -25 -20
161 Ser Pro Arg Val Arg Ala Ala Arg Leu Gly Gly Arg Ala Ala Arg Ser
162 -15 -10 -5 -1 1
163 Gly Ser Gly Gly Ala Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val
164 5 10 15
165 Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu Val Arg Phe Arg
166 20 25 30
167 Phe Cys Thr Gly Ser Cys Pro Arg Ala Arg Ser Pro His Asp Leu Ser
168 35 40 45
169 Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Ala Pro Pro Pro Gly Ser
170 50 55 60
171 Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val
172 65 70 75 80
173 Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val Asp Arg Leu Ser
174 85 90 95
175 Ala Thr Ala Cys Gly Cys Leu Gly
176 100 105
177 <210> SEQ ID NO: 3
178 <211> LENGTH: 861
179 <212> TYPE: RNA
180 <213> ORGANISM: Homo sapiens
181 <220> FEATURE:
182 <221> NAME KEY: 5'UTR
183 <222> LOCATION: 1..117
184 <223> FEATURE:
185 <224> NAME KEY: 3'UTR

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/804,615

DATE: 0815 11 01

TIME: 01:01:40

Input Set : A:\Bgn-111.app

Output Set: N:\CRF3\08132001\I804615.raw

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208 <223> LOCATION: (1)..(6)
210 <224> FEATURE:
211 <224> NAME KEY: CINTR
212 <223> LOCATION: (616)..(661)
214 <224> FEATURE:
215 <224> NAME KEY: sig_peptide
216 <223> LOCATION: (7)..(174)
218 <224> FEATURE:
219 <224> NAME KEY: mat_peptide
220 <223> LOCATION: (298)..(717)
222 <224> FEATURE:
223 <224> NAME KEY: mat_peptide
224 <223> LOCATION: (370)..(717)
226 <224> FEATURE:
227 <224> NAME KEY: mat_peptide
228 <223> LOCATION: (379)..(717)
230 <224> FEATURE:
231 <224> NAME KEY: misc_structure
232 <223> LOCATION: (661)..(663)
233 <223> OTHER INFORMATION: CARBOHYD: glycosylated Asparagine as Asn122
235 <224> FEATURE:
236 <224> NAME KEY: misc_structure
237 <223> LOCATION: (424)..(621)
238 <223> OTHER INFORMATION: DISULFID: Cys43-Cys106 disulfide bridge
240 <224> FEATURE:
241 <224> NAME KEY: misc_structure
242 <223> LOCATION: (503)..(705)
243 <223> OTHER INFORMATION: DISULFID: Cys73-Cys136 disulfide bridge
245 <224> FEATURE:
246 <224> NAME KEY: misc_structure
247 <223> LOCATION: (517)..(711)
248 <223> OTHER INFORMATION: DISULFID: Cys74-Tyr134 disulfide bridge
250 <224> FEATURE:
251 <224> NAME KEY: misc_structure
252 <223> LOCATION: (616)..(616)
253 <223> OTHER INFORMATION: DISULFID: Cys17-Cys137 interchain disulfide
254 bridge
256 <400> SEQUENCE: 5
257 gaaacc atg acc gga atg atc taa ggc cca cca cca cca cca cca cca 47
258 Met Phe Gly Leu Ile Ser Ala Arg Gly Ala Phe Leu Leu Ala
259 -35 -25 -15
261 gtc att cct cca cca gac cca cca ggt acc cca ttt ctc att ggt ggt 50
262 Val Leu Phe Phe Ala Ala His Leu Gly Ala Leu Phe Leu Phe Ala
263 -5 -15 -25
265 cca att att cca ttt cca cca cca cca cca cca cca cca cca cca cca 104
266 Phe Leu Gly Ser Ser Ala Ala Ile Ala Leu Thr Ile Thr Leu Ala Ala
267 -5 -15 -25
269 atg ggt ggt cca cca cca cca cca cca cca cca cca cca cca cca cca 141
270 Leu Ala Leu Leu Ser Ser Val Ala His Ala Ser Leu Gly Ser Ala Phe

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/804,615

DATE: 04-11-2001

TIME: 11:11:46

Input File: A:\Bgn-111.app

Output File: N:\CRF3\08132001\I804615.raw

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271      -53      -45      -4
273 ggc agg act gag ccc ccc gag ggc ccc ccc act ccc ccc ccc ccc ccc 210
274 Arg Ser Pro Ala Pro Arg Gln Gly Pro Ile Ile Val Leu Ala Ser Pro
275 -35      -35      -15      -10
277 gcc ggc gag ctg ccc gag gag ggc gag ccc ccc ccc ccc ccc ccc ccc 220
278 Ala Gly His Leu Pro Gly Gly Arg Thr Ala Arg Thr Cys Ser Gly Arg
279 -13      -13      -5
281 gcc cgg cgg cgg cgg cgg cgg ccc ccc ccc ccc ccc ccc ccc ccc ccc 230
282 Ala Arg Arg Pro Pro Gln Pro Ser Ala Pro Ala Pro Pro Pro Pro
283 -1      1      5      10
285 gca ccc ccc ccc ccc ccc ccc ccc ggc ggc ggc ggc ggc ggc ggc ggc 240
286 Ala Pro Pro Ser Ala Leu Pro Arg Gly Gly Arg Ala Ala Arg Ala Gly
287 15      20      25
289 ggc ccc ggc aac cgc ccc ccc ggc ggc ggc ggc ggc ggc ggc ggc ggc 250
290 Gly Pro Gly Asn Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu
291 30      35      40      45
293 cgc tgc cag ctg gtg cgc gtg cgc ggc ctc ggc ctg ggc cag cgc tcc 260
294 Arg Ser Gln Leu Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser
295 50      55      60
297 gac gag ctg gtg cgt ttc cgc ttc tgc agc ggc tcc tgc cgc cgc ggc 270
298 Asp Gln Leu Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Ala
299 65      70      75
301 cgc tcc cca cag gac ctc agc ctg ggc aga cta ctg ggc gcc ggc gcc 280
302 Arg Ser Pro His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala
303 80      85      90
305 ctg cga ccc ccc ccc ggc tcc cgc ccc ctc agc aga ccc ccc tgc tcc cga 290
306 Leu Arg Pro Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg
307 95      100      105
309 ccc acc cgc tac gaa ggc gtc tcc ttc atg gac gtc aac agc acc tgg 300
310 Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp
311 110      115      120      125
313 aqa acc gtg gac cgc ctc tcc gcc aac ccc tgc ggc tgc ctg ggc 310
314 Arg Thr Val Asp Arg Leu Ser Ala Asn Pro Cys Gly Cys Leu Gly
315 130      135      140
317 agagggtctg ctccagggt ttgcagactg gacccctacc ggtggctctt cctccctggg 320
318 aacctccccc agatccac tagccaggg cctccctccg ggcagagga cctccctcc 330
319 agaggccct gccctgggt gatg 340
324 <210> SEQ ID NO: 4
325 <211> LENGTH: 137
326 <212> TYPE: PRT
327 <213> ORGANISM: Homo sapiens
328 <400> SEQUENCE: 4
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331 -40      -40      -40
333 Pro Pro Gln Ala His Leu Gly Ala Leu Ile Ile Ile Ile Gln Ala Pro Leu
334 -80      -80      -80
336 gly Leu Ser Ala Gln Pro Ala Leu Thr Ile Thr Leu Ala Ala Leu Ala
337 -65      -65      -65
339 Leu Leu Ser Ser Val Ala Gln Ala Ser Leu Gly Ser Ala Pro Arg Ser

```

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/804,615

DATE: 01/14/2001

TIME: 11:11:11

Input Set : A:\Bgn-111.app

Output Set: N:\CRF3\08132001\I804615.raw

L:1 M:275 C: Current Application Number differs, replaced Current Application Number  
 L:411 M:258 W: Mandatory Feature missing, +221 not found for SEQ ID#:1  
 L:411 M:258 W: Mandatory Feature missing, +221 not found for SEQ ID#:1  
 L:411 M:341 W: (46) "r" or "Xaa" used, for SEQ ID#:1  
 L:443 M:258 W: Mandatory Feature missing, +221 not found for SEQ ID#:1  
 L:443 M:258 W: Mandatory Feature missing, +221 not found for SEQ ID#:1  
 L:443 M:341 W: (46) "r" or "Xaa" used, for SEQ ID#:1  
 L:478 M:258 W: Mandatory Feature missing, +221 not found for SEQ ID#:1  
 L:478 M:258 W: Mandatory Feature missing, +221 not found for SEQ ID#:1  
 L:478 M:341 W: (46) "r" or "Xaa" used, for SEQ ID#:1  
 L:1091 M:258 W: Mandatory Feature missing, +221 not found for SEQ ID#:27  
 L:1091 M:258 W: Mandatory Feature missing, +221 not found for SEQ ID#:27  
 L:1091 M:341 W: (46) "r" or "Xaa" used, for SEQ ID#:27